



SEQUENCE LISTING

<110> Alitaid, Kari
Joukov, Vladimir

<120> VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
AND GENE, MUTANTS THEREOF, AND USES THEREOF

<130> 28967/34140A

<140> US 09/534,376

<141> 2000-03-24

<150> 09/355,700

<151> 1999-11-05

<150> PCT/US98/01973

<151> 1998-02-02

<150> 08/795,430

<151> 1997-02-05

<150> PCT/FI96/00427

<151> 1996-08-01

<150> 08/671,573

<151> 1996-06-28

<150> 08/601,132

<151> 1996-02-14

<150> 08/585,895

<151> 1996-01-12

<150> 08/510,133

<151> 1995-08-01

<150> 08/340,011

<151> 1994-11-14

<160> 59

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<223> Human Flt4 cDNA (short form)

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 <213> Homo sapiens

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 <213> Artificial Sequence

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<213> Homo sapiens

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conditioned medium

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Leu Lys

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Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

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Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

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Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
85 90 95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
100 105 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115 120 125 130

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gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
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165 170 175
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 295 300 305

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 tcttgatgatt tctttaaaag aatgactata taattttatt ccaactaaaaa tattgtttct 1898
 gcatttcatt ttatagcaac aacaattggg aaaactcact gtgatcaata tttttatata 1958
 atgcaaaata tgtttaaaat aaaatgaaaa ttgtattat 1997

<210> 8
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15
 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
 20 25 30
 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
 35 40 45
 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
 50 55 60
 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
 65 70 75 80
 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
 85 90 95
 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
 100 105 110
 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125
 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140
 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160
 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175
 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
 180 185 190
 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
 195 200 205
 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
 210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
 225 230 235 240
 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
 245 250 255
 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
 260 265 270
 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
 275 280 285
 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300
 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320
 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335
 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350
 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365
 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380
 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
 385 390 395 400
 Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415
 Gln Met Ser

<210> 9
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <223> VEGF-C peptide "PAM126"

<400> 9
 Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
 1 5 10 15
 Lys

<210> 10
 <211> 1836
 <212> DNA
 <213> Murine

<220>

<221> CDS

<222> (168)...(1412)

<220>

<221> cDNA encoding murine VEGF C precursor

<400> 10

gcgcccggt cgacgcaaaa gttgcgagcc gccgagtcgc gggagacgct cgcgccagggg 60

gggtcccgagg aggaaccac gggacagggg ccaggagagg acctcagcct cagccccag 120

cctgcgcag ccaacggacc ggctccctg ctcccggtcc atccacc atg cac ttg 176
Met His Leu
1

ctg tgc ttc ttg tct ctg gcg tgt tcc ctg ctc gcc gct gcg ctg atc 224
Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala Leu Ile
5 10 15

ccc agt ccg cgc gag gcg ccc gcc acc gtc gcc gcc ttc gag tcg gga 272
Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe Glu Ser Gly
20 25 30 35

ctg ggc ttc tcg gaa gcg gag ccc gac ggg ggc gag gtc aag gct ttt 320
Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val Lys Ala Phe
40 45 50

gaa ggc aaa gac ctg gag gag cag ttg cgg tct gtg tcc agc gta gat 368
Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp
55 60 65

gag ctg atg tct gtc ctg tac cca gac tac tgg aaa atg tac aag tgc 416
Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met Tyr Lys Cys
70 75 80

cag ctg cgg aaa ggc ggc tgg cag cag ccc acc ctc aat acc agg aca 464
Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn Thr Arg Thr
85 90 95

ggg gac agt gta aaa ttt gct gct gca cat tat aac aca gag atc ctg 512
Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
100 105 110 115

aaa agt att gat aat gag tgg aga aag act caa tgc atg cca cgt gag 560
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
120 125 130

gtg tgt ata gat gtg ggg aag gag ttt gga gca gcc aca aac acc ttc 608
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr Asn Thr Phe
135 140 145

ttt aaa cct cca tgt gtg tcc gtc tac aga tgt ggg ggt tgc tgc aac 656
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
150 155 160

agc gag ggg ctg cag tgc atg aac acc agc aca ggt tac ctc agc aag 704
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr Leu Ser Lys
165 170 175

acg ttg ttt gaa att aca gtg cct ctc tca caa ggc ccc aaa cca gtc 752
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
180 185 190 195

aca atc agt ttt gcc aat cac act tcc tgc cgg tgc atg tct aaa ctg 800
 Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
 200 205 210

gat gtt tac aga caa gtt cat tca att att aga cgt tct ctg cca gca 848
 Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala
 215 220 225

aca tta cca cag tgt cag gca gct aac aag aca tgt cca aca aac tat 896
 Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr
 230 235 240

gtg tgg aat aac tac atg tgc cga tgc ctg gct cag cag gat ttt atc 944
 Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln Asp Phe Ile
 245 250 255

ttt tat tca aat gtt gaa gat gac tca acc aat gga ttc cat gat gtc 992
 Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe His Asp Val
 260 265 270 275

tgt gga ccc aac aag gag ctg gat gaa gac acc tgt cag tgt gtc tgc 1040
 Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln Cys Val Cys
 280 285 290

aag ggg ggg ctt cgg cca tct agt tgt gga ccc cac aaa gaa cta gat 1088
 Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys Glu Leu Asp
 295 300 305

aga gac tca tgt cag tgt gtc tgt aaa aac aaa ctt ttc cct aat tca 1136
 Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Asn Ser
 310 315 320

tgt gga gcc aac agg gaa ttt gat gag aat aca tgt cag tgt gta tgt 1184
 Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys
 325 330 335

aaa aga acg tgt cca aga aat cag ccc ctg aat cct ggg aaa tgt gcc 1232
 Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala
 340 345 350 355

tgt gaa tgt aca gaa aac aca cag aag tgc ttc ctt aaa ggg aag aag 1280
 Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys Gly Lys Lys
 360 365 370

ttc cac cat caa aca tgc agt tgt tac aga aga ccg tgt gcg aat cga 1328
 Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Ala Asn Arg
 375 380 385

ctg aag cat tgt gat cca gga ctg tcc ttt agt gaa gaa gta tgc cgc 1376
 Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu Val Cys Arg
 390 395 400

tgt gtc cca tgc tat tgg aaa agg cca cat ctg aac taagatcata 1422
 Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

ccagttttca gtcagtcaca gtcatttact ctcttgaaga ctgttggaac agcacttagc 1482

actgtctatg cacagaaaga ctctgtggga ccacatggta acagaggccc aagtctgtgt 1542

ttattgaacc atgtggatta ctgcgggaga ggactggcac tcatgtgcaa aaaaaacctc 1602

ttcaaagact gggtttctgc cagggaccag acagctgagg tttttctctt gtgatttaaa 1662

aaaagaatga ctatataatt tattttccact aaaaatattg tteetgcatt catttttata 1722
gcaataacaa ttggtaaagc tcactgtgat cagtatTTTT ataacatgca aaactatggt 1782
taaaataaaa tgaaaattgt attataaaaa aaaaaaaaaa aaaaaaaaaa gctt 1836

<210> 11
<211> 415
<212> PRT
<213> Murine

<400> 11
Met His Leu Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Ile Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe
20 25 30
Glu Ser Gly Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val
35 40 45
Lys Ala Phe Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn
85 90 95
Thr Arg Thr Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr
100 105 110
Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met
115 120 125
Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr
130 135 140
Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly
145 150 155 160
Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr
165 170 175
Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro
180 185 190
Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met
195 200 205
Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser
210 215 220
Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro
225 230 235 240
Thr Asn Tyr Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln
245 250 255
Asp Phe Ile Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe
260 265 270

His Asp Val Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln
 275 280 285
 Cys Val Cys Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys
 290 295 300
 Glu Leu Asp Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe
 305 310 315 320
 Pro Asn Ser Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln
 325 330 335
 Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly
 340 345 350
 Lys Cys Ala Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys
 355 360 365
 Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys
 370 375 380
 Ala Asn Arg Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu
 385 390 395 400
 Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

<210> 12
 <211> 1/41
 <212> DNA
 <213> Quail

<220>
 <221> CDS
 <222> (453)..(1706)

<220>
 <223> Quail VEGF-C cDNA

<400> 12
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 gcgagcgcc actgggtcct gettccctcc ttctctccc tctctcct cctccttctc 120
 tctgcgcttt ccacgcctcc cgagcgagcg cacgcctcgga tgccgggtt cctgggtgggt 180
 tttttacctg gcaaagtcg gataacttcg gtgagaattt gcaaagaggc tgggagctcc 240
 cctgcaggcg tctgggagct gctgccgcg tcgcatcttc tccatcccgc ggattttact 300
 gccttgata ttgcgagggg agggaggggg gtgaggacag caaaaagaaa ggggtggggg 360
 gggggagaga aaaggaaaag aaggagcctc ggaattgtgc ccgcattcct gcgctgcccc 420
 gcgaccccc tccgctctgc catctccgca ca atg cac ttg ctg gag atg ctc 473
 Met His Leu Leu Glu Met Leu
 1 5
 tcc ctg ggc tgc tgc ctc gct gct ggc gcc gtg ctc ctg gga ccc cgg 521
 Ser Leu Gly Cys Cys Leu Ala Ala Gly Ala Val Leu Leu Gly Pro Arg
 10 15 20

cag ccg ccc gtc gcc gcc gcc tac gag tcc ggg cac ggc tac tac gag 569
 Gln Pro Pro Val Ala Ala Tyr Glu Ser Gly His Gly Tyr Tyr Glu
 25 30 35

gag gag ccc ggt gcc ggg gaa ccc aag gct cat gca agc aaa gac ctg 617
 Glu Glu Pro Gly Ala Gly Glu Pro Lys Ala His Ala Ser Lys Asp Leu
 40 45 50 55

gaa gag cag ttg cga tct gtg tcc agt gtg gat gaa ctc atg aca gta 665
 Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val
 60 65 70

ctt tac cca gaa tac tgg aaa atg ttc aaa tgt cag ttg agg aaa gga 713
 Leu Tyr Pro Glu Tyr Trp Lys Met Phe Lys Cys Gln Leu Arg Lys Gly
 75 80 85

ggt tgg caa cac aac agg gaa cac tcc agc tct gat aca aga tca gat 761
 Gly Trp Gln His Asn Arg Glu His Ser Ser Ser Asp Thr Arg Ser Asp
 90 95 100

gat tca ttg aaa ttt gcc gca gca cat tat aat gca gag atc ctg aaa 809
 Asp Ser Leu Lys Phe Ala Ala Ala His Tyr Asn Ala Glu Ile Leu Lys
 105 110 115

agt att gat act gaa tgg aga aaa acc cag ggc atg cca cgt gaa gtg 857
 Ser Ile Asp Thr Glu Trp Arg Lys Thr Gln Gly Met Pro Arg Glu Val
 120 125 130 135

tgt gtg gat ttg ggg aaa gag ttt gga gca act aca aac acc ttc ttt 905
 Cys Val Asp Leu Gly Lys Glu Phe Gly Ala Thr Thr Asn Thr Phe Phe
 140 145 150

aaa ccc ccg tgt gta tcc atc tac aga tgt gga ggt tgc tgc aat agt 953
 Lys Pro Pro Cys Val Ser Ile Tyr Arg Cys Gly Gly Cys Cys Asn Ser
 155 160 165

gaa gga ctc cag tgt atg aat atc agc aca aat tac atc agc aag aca 1001
 Glu Gly Leu Gln Cys Met Asn Ile Ser Thr Asn Tyr Ile Ser Lys Thr
 170 175 180

ttg ttt gag att aca gtg cct ctc tct cat ggc ccc aaa cct gta aca 1049
 Leu Phe Glu Ile Thr Val Pro Leu Ser His Gly Pro Lys Pro Val Thr
 185 190 195

gtc agt ttt gcc aat cac acg tcc tgc cga tgc atg tct aag ttg gat 1097
 Val Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp
 200 205 210 215

gtt tac aga caa gtt cat tct atc ata aga cgt tcc ttg cca gca aca 1145
 Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr
 220 225 230

caa act cag tgt cat gtg gca aac aag acc tgt cca aaa aat cat gtc 1193
 Gln Thr Gln Cys His Val Ala Asn Lys Thr Cys Pro Lys Asn His Val
 235 240 245

tgg aat aat cag att tgc aga tgc tta gca cag cac gat ttt ggt ttc 1241
 Trp Asn Asn Gln Ile Cys Arg Cys Leu Ala Gln His Asp Phe Gly Phe
 250 255 260

tct tct cac ctt gga gat tct gac aca tct gaa gga ttc cat att tgt 1289
 Ser Ser His Leu Gly Asp Ser Asp Thr Ser Glu Gly Phe His Ile Cys
 265 270 275

ggg ccc aac aaa gag ctg gat gaa gaa acc tgt caa tgc gtc tgc aaa 1337
 Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Lys
 280 285 290 295
 gga ggt gtg cgg ccc ata agc tgt ggc cct cac aaa gaa cta gac agg 1385
 Gly Gly Val Arg Pro Ile Ser Cys Gly Pro His Lys Glu Leu Asp Arg
 300 305 310
 gca tca tgt cag tgc atg tgc aaa aac aaa ctg ctc ccc agt tcc tgt 1433
 Ala Ser Cys Gln Cys Met Cys Lys Asn Lys Leu Leu Pro Ser Ser Cys
 315 320 325
 ggg cct aac aaa gaa ttt gat gaa gaa aag tgc cag tgt gta tgt aaa 1481
 Gly Pro Asn Lys Glu Phe Asp Glu Glu Lys Cys Gln Cys Val Cys Lys
 330 335 340
 aag acc tgt ccc aaa cat cat cca cta aat cct gca aaa tgc atc tgc 1529
 Lys Thr Cys Pro Lys His His Pro Leu Asn Pro Ala Lys Cys Ile Cys
 345 350 355
 gaa tgt aca gaa tct ccc aat aaa tgt ttc tta aaa gga aaa aga ttt 1577
 Glu Cys Thr Glu Ser Pro Asn Lys Cys Phe Leu Lys Gly Lys Arg Phe
 360 365 370 375
 cat cac cag aca tgc agt tgt tac aga cca cca tgt aca gtc cga acg 1625
 His His Gln Thr Cys Ser Cys Tyr Arg Pro Pro Cys Thr Val Arg Thr
 380 385 390
 aaa cgc tgt gat gct gga ttt ctg tta gct gaa gaa gtg tgc cgc tgt 1673
 Lys Arg Cys Asp Ala Gly Phe Leu Leu Ala Glu Glu Val Cys Arg Cys
 395 400 405
 gta cgc aca tct tgg aaa aga cca ctt atg aat taagcgaaga aagcactact 1726
 Val Arg Thr Ser Trp Lys Arg Pro Leu Met Asn
 410 415
 cgctatatag tgctcg 1741

<210> 13
 <211> 418
 <212> PRT
 <213> Quail

<400> 13
 Met His Leu Leu Glu Met Leu Ser Leu Gly Cys Cys Leu Ala Ala Gly
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 20 25 30
 Ser Gly His Gly Tyr Tyr Glu Glu Glu Pro Gly Ala Gly Glu Pro Lys
 35 40 45
 Ala His Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser
 50 55 60
 Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Phe
 65 70 75 80
 Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu His Ser
 85 90 95

Ser Ser Asp Thr Arg Ser Asp Asp Ser Leu Lys Phe Ala Ala Ala His
 100 105 110
 Tyr Asn Ala Glu Ile Leu Lys Ser Ile Asp Thr Glu Trp Arg Lys Thr
 115 120 125
 Gln Gly Met Pro Arg Glu Val Cys Val Asp Leu Gly Lys Glu Phe Gly
 130 135 140
 Ala Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Ile Tyr Arg
 145 150 155 160
 Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Ile Ser
 165 170 175
 Thr Asn Tyr Ile Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser
 180 185 190
 His Gly Pro Lys Pro Val Thr Val Ser Phe Ala Asn His Thr Ser Cys
 195 200 205
 Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
 210 215 220
 Arg Arg Ser Leu Pro Ala Thr Gln Thr Gln Cys His Val Ala Asn Lys
 225 230 235 240
 Thr Cys Pro Lys Asn His Val Trp Asn Asn Gln Ile Cys Arg Cys Leu
 245 250 255
 Ala Gln His Asp Phe Gly Phe Ser Ser His Leu Gly Asp Ser Asp Thr
 260 265 270
 Ser Glu Gly Phe His Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu
 275 280 285
 Thr Cys Gln Cys Val Cys Lys Gly Gly Val Arg Pro Ile Ser Cys Gly
 290 295 300
 Pro His Lys Glu Leu Asp Arg Ala Ser Cys Gln Cys Met Cys Lys Asn
 305 310 315 320
 Lys Leu Leu Pro Ser Ser Cys Gly Pro Asn Lys Glu Phe Asp Glu Glu
 325 330 335
 Lys Cys Gln Cys Val Cys Lys Lys Thr Cys Pro Lys His His Pro Leu
 340 345 350
 Asn Pro Ala Lys Cys Ile Cys Glu Cys Thr Glu Ser Pro Asn Lys Cys
 355 360 365
 Phe Leu Lys Gly Lys Arg Phe His His Gln Thr Cys Ser Cys Tyr Arg
 370 375 380
 Pro Pro Cys Thr Val Arg Thr Lys Arg Cys Asp Ala Gly Phe Leu Leu
 385 390 395 400
 Ala Glu Glu Val Cys Arg Cys Val Arg Thr Ser Trp Lys Arg Pro Leu
 405 410 415
 Met Asn

<210> 14
<211> 10
<212> PPT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<229>
<223> IgG-Kappa sequence

<400> 14
Ala Val Val Met Thr Gln Thr Pro Ala Ser
1 5 10

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 15 22
tctcttctgt gcttgagttg ag

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16 22
tctcttctgt ccttgagttg ag

<210> 17
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 17 65
tgtgtgcag caaattttat agtctcttct gtggcgggcg cgcgggcgga cgcctcgca 60
ggacc

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 18 30
ctggcaggga actgctaata atggaatgaa

<210> 19
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 19 60
gggtccggg tccgagaggt cgagtcggga ctggtgatgg tgatggtgat gggcggcggc
ggcggcgggc gctcggcggg gacc 84

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 20 31
gtattataat gtctccacc aaattttata g

<210> 21
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21 93
gttcgctgcc tgacactgtg gtagtggtgc tggcggccgc tagtgatggt gatggtgatg
ataatggaa tgaacttgtc tgtaaacatc cag

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22 17
catgtacgaa ccgccag

<210> 23

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
aatgacacaga gagaggcgag 20

<210> 24
<211> 24
<212> DNA
<213> Homo sapiens

<400> 24
ggcagaggcca cggtaggtct gcgt 24

<210> 25
<211> 24
<212> DNA
<213> Homo sapiens

<400> 25
ttctcttgac aggcattatgc aagc 24

<210> 26
<211> 24
<212> DNA
<213> Homo sapiens

<400> 26
gagatcttga aaagtaagta tggg 24

<210> 27
<211> 23
<212> DNA
<213> Homo sapiens

<400> 27
atgacttgac aggtattgat aat 23

<210> 28
<211> 23
<212> DNA
<213> Homo sapiens

<400> 28
ctcagcaaga cggtaggtat tgt 23

<210> 29
<211> 25
<212> DNA
<213> Homo sapiens

<400> 29
cccttctttg tagttatttg aaatt 25

<210> 30
<211> 31
<212> DNA
<213> Homo sapiens

<400> 30
atgctatccac agtgagtatg aattaaa

27

<210> 31
<211> 34
<212> DNA
<213> Homo sapiens

<400> 31
ttctttcctaaa ggtgtcaggc agcg

24

<210> 32
<211> 31
<212> DNA
<213> Homo sapiens

<400> 32
gctggagatg gtagcagaat g

21

<210> 33
<211> 23
<212> DNA
<213> Homo sapiens

<400> 33
ctatttgtct agactcaaca gat

23

<210> 34
<211> 22
<212> DNA
<213> Homo sapiens

<400> 34
caaacatgca ggtaagagat cc

22

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
tgttttctcta gctgttacag acgg

24

<210> 36
<211> 24
<212> DNA
<213> Murine

<400> 36
ggcaggtca aggtaggtgc aagg

24

<210> 37
<211> 26
<212> DNA
<213> Murine

<400> 37
attgtctttg acaggctttt tgaagg

26

<210> 38
<211> 21
<212> DNA
<213> Murine

<400> 38
gagatcttga aaagtaagta g

21

<210> 39
<211> 24
<212> DNA
<213> Murine

<400> 39
tgtgactcga caggtattga taat

24

<210> 40
<211> 20
<212> DNA
<213> Murine

<400> 40
ctcaggaaga cggtaggtat

20

<210> 41
<211> 25
<212> DNA
<213> Murine

<400> 41
ttgtcccttg tagttgtttg aaatt

25

<210> 42
<211> 20
<212> DNA
<213> Murine

<400> 42
acattaccac agtgagtatg

20

<210> 43
<211> 26
<212> DNA
<213> Murine

<400> 43
gtctccccaa aagggtgtcag gcagct

26

<210> 44
<211> 23
<212> DNA
<213> Murine

<400> 44
aatgttgaag atggttaagta aaa

23

<210> 45
<211> 16
<212> DNA
<213> Murine

<400> 45
tetagactca accaat

16

<210> 46
<211> 22
<212> DNA
<213> Murine

<400> 46
caaacatgca ggtaaggagt gt

22

<210> 47
<211> 24
<212> DNA
<213> Murine

<400> 47
ttttcccta gttgttacag aaga

24

<210> 48
<211> 2991
<212> DNA
<213> Homo sapiens

<220>
<223> Genomic DNA - Sequence upstream of VEGF-C coding
sequence

<400> 48
gttttaagta gagacggggt ttcaccaacg gttgaaaata tttatcatgg tctccctaag 60
atgyacgggtg ttagctagga tggctcgcgt ctctgacct catgatccac ccgcctcggc 120
ctctcaaaagt gctgggatta caggcgtgag ccaccgtgct cgaccaacct taagacaaac 180
aactactgca tgattgtttt tggagacctt tttttatctt aaataaattt ttgccagcat 240
tttctgactc aaagtatagc agcaggaaga taacactttt gtgagaaaaa agtttgaata 300
cagcttactg ctgtatttaa atgaaacagt agttaatatg atattaatat attttggata 360
tattttgagt ttgttgattt tccagctctc acccgtgct aggctgtgg gtgttggaag 420
tgctgtggtt tctcaatttt gtttgctat tagaatctg atgtccaagc cttactccag 480
ttagaccagt taagccagaa aggcagaagg tgtactcaag catctgtttt ttcaaaatct 540

ccttttgtga tgcgaagtgc aatcaaaagtt tagaatcatt gtaataagcaa atgggttgaat 600
 ggaaaactcca cctttctatc aaatcctacc ccagttctgcc cttagctgtt ctcttttccac 660
 agatctatca atgtctgaag ataactatgg caggtctgac aaatatgcac agagcaggaa 720
 gacagcaaga gagtatgaca ctgaccatgt tccaaatcac aaaacatctc aacaggctag 780
 atcatggacc gagtctgatg ggatggaatt tcataaagat acataaaaaa gcattcttga 840
 tacagtaaac ttaactccac aaatacaggg gaatttagac gtgactaagt agcagtcacat 900
 atgaaaaatt attgaggaat ttgtttgact ttaagggtag tgtgagtcaa cactgtgatt 960
 tggctgccag aaaataaact caatccaagg ctgtatcaac aaaggcatac tgtccattct 1020
 gcattctcat tacagcacta agtaccgagc catgtttctc accgcatact tcatgaacat 1080
 ggaaagctaa cagtatgggt aaggggggaa actggaactg tcatcttggg gaataaaagg 1140
 gatatttagc caggagtaaa gttagcttag ggagaccatg ataaatattt tcaaaatatt 1200
 tgaaggactc agttgtggaa gtgagattag atttattgtg taaaactcca ggagtcaaaa 1260
 gcaatagaga gatagaagga aatgcttttc agcagtgttg ctcatcaata aaggagtgta 1320
 acagccacac agaattggaag gttccctgtc ctttgagata tttaagcctt caagtaaat 1380
 atgggtgagg agtttcaaat ctgagttga accagataag aaagtctctt ctcccggtta 1440
 gatattatgg acctataaca tctgttact taaaagtaga ttgggagtga aaggcagact 1500
 tttgatgttc tgtacactgt tgaaacctt tagcgtggtc ctctgtaacc tgcacacct 1560
 gccccaaagg ggcagctagc caatgccacc agcccaacgg aaaccccagt gcttttccaa 1620
 tggggaaatg cagtcacttt tctttggatg ctacacatcc tttctggaat atgtctcaca 1680
 cacatctctc tttatcacc cctttttcaa gtaaaccaac ttcttgaga agctgacaat 1740
 gtgtctcttt actctccacg aagattctgg cctttctctt cacctgtcag aagtttagga 1800
 ttccaaaggg atcattagca tccatcccaa cagcctgcac tgcacctga gaactgcggt 1860
 tcttgatca tcaggcaact ttcaactaca cagaccaagg gagagagggg accctccga 1920
 ggtcccatag ggttctctga catagtgatg acctttttcc aaactttgag cagggcgctg 1980
 ggggcagggc gtgcgggagg gaggacaaga actcgggagt ggccgaggat aaagcggggg 2040
 ctccctccac cccacgggtc ccagtttctc cccgtgcac gtggtccagg gtggctgcac 2100
 cacctctaaa gccgggtccc ccaaccgcca gccccgggac tgaacttgcc cctccggccg 2160
 cccgtctccc gcaggggaca ggggcgggga gggagagatc cagagggggg ctgggggagg 2220
 tggggccgcc ggggaggagg cgagggaaac ggggagctcc agggagacgg ctccgaggg 2280
 agagttagag gggagggcag cccgggctcg gcacgtccc tccctcggcc gctttctctc 2340
 acataagcgc aggcagaggg ccggtcagtc atgcctgcc cctgcgcccg ccgccgcgc 2400
 cgccgcgct cagcccgccg ccgtctggag gactctgcgc cggggcgctc cggggcccg 2460

ccgagggcag cggccccggc ggccctctct cggccccggg caccggcggc agcggccccg 2520
 ccgagggcgc cggggccggg ctctctctac ttgggggaag gggagggagg agggggacga 2580
 ggggtctggg ggggttgagg gggtgaaca tcggggggtg ttctggtgtc cccgccccg 2640
 ctctctcaaa aagctacacc gacggggacc ggggggggtt cctccctggc cctcgcttca 2700
 cctcgggggc tcgaatggg gggagctcgg atgtccgggtt tctgtgagg cttttacctg 2760
 aatccggcgc cctttccccg gcactggctg ggagggcgcc ctgcaaagtt gggaacgcgg 2820
 agcccgaggc ccgctccggc cgcctccggc tcgccaggg ggggtcggcg ggaggagccc 2880
 gggggagagg gaccaggagg gggccggcgc ctgcagggg cggccgcggc cccacccctg 2940
 ccccgccag cggaccggtc cccaccccc ggtccttcca ccatgcactt g 2991

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

400 - 49 20
 cagggttat gcaagcaaag

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

400 - 50 20
 aacacagttt tcataatag

<210> 51
 <211> 19
 <212> PRT
 <213> Homo sapiens

400 - 51
 Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu Pro His Glu Leu
 1 5 10 15

His Val Glu

<210> 52
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <225> Description of Artificial Sequence:
 oligonucleotide

<400> 52
 gatggacaca gatggaggtt taaag

25

<210> 53
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human PDGF-A

<400> 53
 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
 1 5 10 15
 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
 20 25 30
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

<210> 54
 <211> 241
 <212> PRT
 <213> Homo sapiens

<220>

<223> Human PDGF B

<400> 54

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
1 5 10 15

Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
20 25 30

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
35 40 45

His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
50 55 60

Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
65 70 75 80

Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
85 90 95

Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
100 105 110

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
115 120 125

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
130 135 140

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
145 150 155 160

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
165 170 175

Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
180 185 190

Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
195 200 205

Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
210 215 220

Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225 230 235 240

Ala

<210> 55

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<223> Human PIGF

<400> 55

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
130 135 140

Ala Val Pro Arg Arg
145

<210> 56

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF165 precursor

<400> 56

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 57

<211> 188

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF-B167

<400> 57

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
 130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185

<210> 58

<211> 419

<212> PPT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: VEGF C delta Cys156 mutant

<220>
<223> At position 156, "Xaa" can be anything other than cysteine or can be nothing

<400> 58
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125
Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140
Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Xaa Val Ser Val Tyr
145 150 155 160
Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175
Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190
Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205
Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220
Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240
Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255
Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270
Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
 385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415

Gln Met Ser

<210> 59

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VEGF-C delta N delta CHis

<400> 59

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Thr
 20 25 30

Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
 35 40 45

Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 50 55 60

Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr Phe
 65 70 75 80

Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
 85 90 95

Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys
 100 105 110

Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
 115 120 125

Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
130 135 140

Asp Val Tyr Arg Gln Val His Ser Ile Ile His His His His His His
145 150 155 160